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Sequence Listing could not be accepted.

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Reviewer: markspencer

Timestamp: [year=2008; month=1; day=14; hr=15; min=46; sec=57; ms=575;]

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Reviewer Comments:

The file contains non-ASCII characters in the Header. Please remove all
non-ASCII characters.

Application No: 10573229

Version No: 1.0

Input Set:

Output Set:

Started: 2008-01-14 14:01:13.086

Finished: 2008-01-14 14:01:19.929

Elapsed: 0 hr(s) 0 min(s) 6 sec(s) 843 ms

Total Warnings: 134

Total Errors: 0

No. of SeqIDs Defined: 312

Actual SeqID Count: 312

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28)
W 213	Artificial or Unknown found in <213> in SEQ ID (31)
W 213	Artificial or Unknown found in <213> in SEQ ID (32)
W 213	Artificial or Unknown found in <213> in SEQ ID (35)
W 213	Artificial or Unknown found in <213> in SEQ ID (36)
W 213	Artificial or Unknown found in <213> in SEQ ID (39)
W 213	Artificial or Unknown found in <213> in SEQ ID (40)

Input Set:

Output Set:

Started: 2008-01-14 14:01:13.086
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Elapsed: 0 hr(s) 0 min(s) 6 sec(s) 843 ms
Total Warnings: 134
Total Errors: 0
No. of SeqIDs Defined: 312
Actual SeqID Count: 312

Error code

Error Description

This error has occurred more than 20 times, will not be displayed

<210> 1
 <211> 920
 <212> DNA
 <213> Homo sapiens

<400> 1
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 tgagccactt tggaagctga tcttgaggca ccagtcaagc ccttagctgg ctgcagccac 180
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 tggagtga aa actttaaggg gctgtccagc taaacctcca acctccagat cccatgccaa 480
 tttctctgct tctgcaaaag gacttcaagt gaaagacatc tgcagctgtg aacgggggta 540
 aaacctccc tgccccaggc cccaagcaag gatttcccta gcggggagga aggtagaatc 600
 gagagacctc taacctggg agaggaggga gggaaatctc cgaggaccag ggttatgcaa 660
 caacacaagg gaagtacctg ctgggttctg ggggttgggg aaggaaaatc cctactgcc 720
 caagagccag cccgaaccc aaggcacagc ttatactggc cccggggcct gggggggcac 780
 gaaaaccttg aaaaaggggc gccttcccag cttccccggg ggtaagggtt ttacccccca 840
 gagggggggg gaaaaatccg agtgggatct ttccaaccg ccgaagacta aaacctttaa 900
 acccccaaag aaaccttcta 920

<210> 2
 <211> 88
 <212> PRT
 <213> Homo sapiens

<400> 2

Arg Arg Phe Leu Trp Gly Phe Lys Gly Phe Ser Leu Arg Arg Leu Gly
 1 5 10 15

Lys Ile Pro Leu Gly Phe Phe Pro Pro Pro Leu Gly Gly Lys Ala Leu
 20 25 30

Thr Pro Gly Glu Ala Gly Lys Ala Pro Leu Phe Gln Gly Phe Arg Ala
 35 40 45

Pro Pro Gly Pro Gly Ala Ser Ile Ser Cys Ala Leu Gly Ser Gly Leu
50 55 60

Ala Leu Gly Ala Val Gly Ile Phe Leu Pro Gln Pro Pro Glu Pro Ser
65 70 75 80

Arg Tyr Phe Pro Cys Val Val Ala
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<210> 3
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 3
gcagccacag ccaacaacaa ga 22

<210> 4
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 4
acagcagagg tgctcctgtc tcttg 25

<210> 5
<211> 2856
<212> DNA
<213> Homo sapiens

<400> 5
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gggaatgggg ggatgatcat tctaattcaa gtggatgcc aactccacac ccccggttac 180
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tctcaggtta	acttcaccac	caaagcccaa	gaagaggttt	tcttcgcca	agatggggaa	2100
gtgctgacaa	cgtttgacat	taaaaacatc	tatgttctcc	cagacctgtc	aggacagaca	2160

gccattgttg gacactttga cttcagagca ctttctggaa aagagcttct gttggatgac 2220
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<210> 6
<211> 951
<212> PRT
<213> Homo sapiens

<400> 6

Met Ala Lys Arg Asn Leu Ser Thr Val Thr Glu Phe Ile Leu Val Val
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Phe Thr Asp His Pro Glu Leu Ala Val Pro Leu Phe Leu Val Phe Leu
20 25 30

Ser Phe Tyr Leu Val Thr Phe Leu Gly Asn Gly Gly Met Ile Ile Leu
35 40 45

Ile Gln Val Asp Ala Gln Leu His Thr Pro Val Tyr Phe Phe Leu Ser
50 55 60

His Leu Ala Phe Leu Asp Ala Cys Cys Ala Ser Val Ile Thr Pro Gln
65 70 75 80

Ile Leu Ala Thr Leu Ala Thr Asp Lys Thr Val Ile Ser Tyr Gly Cys
85 90 95

Arg Ala Val Gln Phe Ser Phe Phe Thr Ile Cys Ala Gly Thr Glu Cys
100 105 110

Tyr Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Ser Asn
115 120 125

Pro Leu His Cys Asn Met Thr Met Thr Pro Gly Thr Cys Arg Val Phe
130 135 140

Leu Ala Ser Ala Phe Ile Cys Gly Val Ser Gly Ala Ile Leu His Thr
145 150 155 160

Thr Cys Thr Phe Thr Leu Ser Phe Cys Cys Asp Asn Gln Ile Asn Phe
165 170 175

Phe Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Ala Cys Ser Ser Met
180 185 190

Thr Gln Thr Glu Ile Val Ile Leu Leu Cys Ala Lys Cys Met Phe Leu
195 200 205

Ala Asn Val Met Val Ile Leu Ile Cys Tyr Met Leu Ile Ile Arg Ala
210 215 220

Ile Leu Arg Val Lys Ser Ala Gly Gly Leu Leu Ile Ala Ser Ala His
225 230 235 240

Phe Asp Ala Tyr Val Tyr Glu Thr Gly Ile Asn Tyr Asn Thr Val Tyr
245 250 255

Gly Ser Gly Lys Ala Val Gly Trp Ser Trp Arg Ser Leu Arg Glu Thr
260 265 270

Asn His Met Arg Pro Gly Asn Thr Ser Lys His Ser Ala Ala Gln Leu
275 280 285

His Gln Cys Leu Ile Gln Gln Val Gly Arg Trp Pro Leu Gln Ser Met
290 295 300

Pro Phe Pro Val Ser Ala Gly Pro Pro Tyr Lys Ser Val Gln Pro Leu
305 310 315 320

Pro Gly Asp Pro Arg Pro Leu Leu Cys Ile Thr Gly Leu Phe Leu Thr

325	330	335
Leu Lys Met Met Gly Cys Gly Pro Arg Arg Pro Arg Asp Arg Lys Ser		
340	345	350
Asp Phe Phe Ile Asn Thr Asp Pro Gly Ala Gly Ser Pro Glu Glu Gln		
355	360	365
Arg Cys Gly Trp Glu Gly His Pro Ser His Ser Tyr Thr Leu Gly Leu		
370	375	380
Ser Leu Pro Val Asn Phe Gly Leu Lys Cys Pro Trp Trp Thr Leu Ser		
385	390	400
Gly Pro Pro Ala Thr Cys Gln Arg Pro Asp Leu Gln Thr Pro Ser Pro		
405	410	415
Pro Lys Glu Ile Cys Ser Ser Gly Leu Arg Pro Leu Thr His Ser Ala		
420	425	430
Gly Pro Asp Arg Ser Gln Val Pro Ala Ala Ser Gly Ala Ala Thr Met		
435	440	445
Leu Thr Lys Gly Leu Pro Asp Ile Thr Val Gly Leu Gln Ile Tyr Asp		
450	455	460
Ser Cys Ile Ser Gly Ile Gln Ala Leu Gly Ser Thr Leu Ala Leu Leu		
465	470	475
Ser Asn Gln Leu Pro Pro Thr Thr Asn Tyr Ala Cys Gly Ser Gln Gln		
485	490	495
His Leu Leu Gly Val Val Gly Gly Met Thr Phe Leu Glu Ser Glu Pro		
500	505	510
Met Ser Glu Leu Leu Ser Ile Tyr Arg Val Pro Gln Gly Gln Arg Leu		
515	520	525
Thr Lys Asn Phe Glu Val Lys Glu Leu Val Cys Thr Tyr Leu Val Gly		
530	535	540
Gln Leu Pro Tyr Gly Leu Val Ser Tyr Asp Asn Ser Asn Phe Glu Trp		
545	550	555
		560

Leu Asp Gln Gln Leu Gln Lys Gln Ile Gly Gly Glu Gly Leu Pro Val
565 570 575

Gly Ala Ala Pro Ser Arg Val Ala Arg Gln Gln Ser Asp Glu Glu Ala
580 585 590

Val Gly Gly Val Gln Gly Tyr Arg Trp Ser Gly Leu Gly Ala Ser Ile
595 600 605

Gln Ser Ala Arg Glu Gly Ala Trp His Arg Thr Gly Leu Glu Asn Met
610 615 620

Thr Thr Ala His Leu Ser Ala Phe Lys Leu Pro Asp Leu Thr Ala Thr
625 630 635 640

Tyr Gln Ala Tyr Leu Ala Ala Lys Ala Leu Trp Val Ala Tyr Gln Asn
645 650 655

Leu Met Ser Cys Ser Glu Arg Glu Gly Pro Phe Leu Gly Gly Thr Tyr
660 665 670

Ala Asn Ala Trp Glu Ala Arg Leu Ser Gln Val Asn Phe Thr Thr Lys
675 680 685

Ala Gln Glu Glu Val Phe Phe Ala Lys Asp Gly Glu Val Leu Thr Thr
690 695 700

Phe Asp Ile Lys Asn Ile Tyr Val Leu Pro Asp Leu Ser Gly Gln Thr
705 710 715 720

Ala Ile Val Gly His Phe Asp Phe Arg Ala Pro Ser Gly Lys Glu Leu
725 730 735

Leu Leu Asp Asp Ser Ala Ile Val Trp Ala Glu Gly Pro Leu Lys Ile
740 745 750

Arg Ala Glu Arg Thr Leu Arg Thr Lys Thr Thr Gln His Leu Ser His
755 760 765

Pro Lys Leu Gln Glu Ser Leu Pro Leu Ser Ala Thr Lys Asn Val Leu
770 775 780

Trp Lys Pro Gly Ser Gln Pro Tyr Leu Arg Ser Gln Asn Ala Ala Thr
785 790 795 800

Lys Ala Phe Pro Asp Pro Glu Glu Lys Ser Gln Cys His Gln Phe Leu
805 810 815

Phe Leu Pro Ser Asp Ser Val Ala Cys Gln Lys Cys Ser Asp Asn Gln
820 825 830

Trp Pro Asn Val Gln Lys Gly Glu Cys Ile Pro Lys Thr Leu Asp Phe
835 840 845

Leu Phe Tyr His Lys Pro Leu Asp Thr Ala Leu Ala Val Cys Thr Ala
850 855 860

Leu Leu Phe Leu Leu Ala Leu Ala Ile Leu Gly Ile Phe His Val Val
865 870 875 880

Cys Ser Cys Val Trp Val Ser Phe Ile Pro Ala His Met His Ala His
885 890 895

Ser Lys Asp Thr Met Ala Met Glu Val Phe Val Ile Leu Ala Ser Ala
900 905 910

Gly Gly Leu Met Ser Ser Leu Phe Phe Ser Lys Cys Tyr Ile Ile Leu
915 920 925

Leu His Pro Glu Lys Asn Thr Lys Asp Gln Met Phe Gly Arg His His
930 935 940

Arg Lys Trp Glu Lys Leu Lys
945 950

<210> 7
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 7
aggtggtgtg acgctgctgc ta

<210> 8
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 8
tcttcttggg ctttggtggt ga 22

<210> 9
<211> 543
<212> DNA
<213> Homo sapiens

<400> 9
ataaagcggg acaacacaga acttcccagt tacaccaggc atcctggccc aaagtttccc 60
aatccaggc ggctagaggc ccaactgcttc ccaactacca gctgaggggg tccgtcccga 120
gaagggagaa gaggccgaag aggaaacatg aacttctatt tactcctagc gagcagcatt 180
ctgtgtgcct tgattgtctt ctggaaatat cgccgctttc agagaaacac tggcgaaatg 240
tcatcaaatt caactgctct tgcactagtg agaccctctt cttctgggtt aattaacagc 300
aatacagaca acaatcttgc agtctacgac ctctctcggg atattttaaa taatttccca 360
cactcaatag ccaggcagaa gcgaatattg gtaaacctca gtatggtgga aaacaagctg 420
gttgaactgg aacatactct acttagcaag ggtttcagag gtgcatcacc tcaccggaaa 480
tccacctaaa agcgtacagg atgtaatgcc agtggtggaa atcattaaag acactttgag 540
tag 543

<210> 10
<211> 113
<212> PRT
<213> Homo sapiens

<400> 10

Met Asn Phe Tyr Leu Leu Leu Ala Ser Ser Ile Leu Cys Ala Leu Ile
1 5 10 15

Val Phe Trp Lys Tyr Arg Arg Phe Gln Arg Asn Thr Gly Glu Met Ser
20 25 30

Ser Asn Ser Thr Ala Leu Ala Leu Val Arg Pro Ser Ser Ser Gly Leu
35 40 45

Ile Asn Ser Asn Thr Asp Asn Asn Leu Ala Val Tyr Asp Leu Ser Arg
50 55 60

Asp Ile Leu Asn Asn Phe Pro His Ser Ile Ala Arg Gln Lys Arg Ile
65 70 75 80

Leu Val Asn Leu Ser Met Val Glu Asn Lys Leu Val Glu Leu Glu His
85 90 95

Thr Leu Leu Ser Lys Gly Phe Arg Gly Ala Ser Pro His Arg Lys Ser
100 105 110

Thr

<210> 11
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 11
gtgtgccttg attgtcttct gg 22

<210> 12
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 12
cctggctatt gagtgtggg 19

<210> 13
<211> 2761
<212> DNA
<213> Homo sapiens

<400> 13
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ccctgaaacc tgcgaggggc ttccgtccac gtccccagtg gacctaccac ccctccatct 180

gggaaagcag gccacagcag ccggacaaag gaagctcttc agcctctagt cgcctctctg 240

tgcattcaca tcggtcactg atctcgcta ctggcacaga cgtgtttatc ggccaaactg 300

ac